Table S1: List of 121 defence-related genes analysed for diurnal and circadian transcriptional regulation using publically available microarray data. *CCA1* and *LHY* are included as known genes subject to circadian regulation.

LOCUS ID	GENE NAME	FUNCTION	REFS
AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1 (CCA1)	MYB transcription factor, CCA1 and LHY function synergistically in regulating circadian rhythms of Arabidopsis	[1 2]
AT1G01060	LATE ELONGATED HYPOCOTYL (LHY)	As above	[1 2]
AT2G14610	PATHOGENESIS-RELATED GENE 1 (PR1)	expression is induced in response to a variety of pathogens and SA. It is a useful molecular marker for the systemic acquired resistance (SAR) response.	[3 4 5]
AT3G57260	PR2	beta 1,3-glucanase, systemic acquired resistance	[5]
AT1G75040	PR5	Thaumatin-like protein involved in response to pathogens.	[5]
AT1G08450	CALRETICULIN 3 (CRT3)	non-receptor component required for EFR-mediated immunity. defense response to bacterium	[6]
AT5G64930	CONSTITUTIVE EXPRESSION OF PR GENES 5 (CPR5)	regulator of expression of PR genes. Participates in signal transduction pathways involved in plant defense (SAR).	[7 8 9]
AT4G39030	ENHANCED DISEASE SUSCEPTIBILITY 5 (EDS5);SA INDUCTION DEFICIENT 1 (SID1)	orphan multidrug and toxin extrusion transporter. Essential component of salicylic acid-dependent signaling for disease resistance. Member of the MATE-transporter family. Expression induced by salicylic acid	[10]
AT1G74710	EDS16 / ISOCHORISMATE SYNTHASE 1 (ICS1)	SA biosynthesis	[11]
AT3G48090	EDS1	encodes lipase-like protein that function in resistance (R) gene-mediated and basal plant disease resistance, required for accumulation of salicylic acid	[12 13]
AT1G64280	NON-EXPRESSER OF PR GENES 1 (NPR1)	Key regulator of SA-mediated signaling	[14]
AT3G52430	PHYTOALEXIN DEFICIENT 4 (PAD4)	encodes lipase-like protein that function in resistance (R) gene-mediated and basal plant disease resistance, required for accumulation of salicylic acid	[12 15 16]
AT4G23100	PAD2 / GLUTAMATE-CYSTEINE LIGASE (GSH1)	catalyzes the first, and rate-limiting, step of glutathione biosynthesis.	[17 18]
AT3G53260	PAL2	phenylpropanoid biosynthesis, SA biosynthesis	[19 20]
AT5G04230	PAL3	as above	[19 20]
AT3G10340	PAL4	as above	[20 21]
AT5G15410	DEFENSE NO DEATH 1 (DND1)	conducts Ca2+ into cells which is linked to the generation of NO and the NO signaling pathway involved in the innate immune	[22]

		response to pathogens defense response	
AT1G08720	ENHANCED DISEASE RESISTANCE 1 (EDR1)	confers resistance to powdery mildew disease caused by the fungus Erysiphe cichoracearum, response to bacterium	[23] [24]
AT2G31880	SUPPRESSOR OF BIR1 1 (SOBIR1)	leucine rich repeat transmembrane protein that is expressed in response to Pseudomonas syringae. positive regulation of defense response	[25]
AT5G10380	RING1	RING finger domain protein with E3 ligase activity. Expression is increased in response to fungal pathogen.	[26]
AT5G46330	FLAGELLIN-SENSITIVE 2 (FLS2)	essential in the perception of flagellin, involved in MAPK signalling relay involved in innate immunity.	[27]
AT5G20480	EF-TU RECEPTOR (EFR)	LRR receptor kinase (LRR-RLK). Functions as the receptor for bacterial PAMP (pathogen associated molecular patterns) EF-Tu	[28]
AT3G21630	Chitin Elicitor Receptor Kinase 1 (CERK1)	LysM receptor-like kinase. Essential in the perception and transduction of the chitin oligosaccharide elicitor. Involved in chitin-mediated plant innate immunity. Located in the plasma membrane.	[29]
AT3G11820	PENETRATION (PEN)-1 / SYNTAXIN OF PLANTS 121 (SYP121)	plasma membrane localized syntaxin, member of the SNARE superfamily proteins, Required for MLO resistance, SA mediated signaling pathway	[30] [31] [32] [33]
AT2G44490	PEN2	peroxisomal glucosyl hydrolase, component of an inducible preinvasion resistance mechanism. Required for MLO resistance.	[34]
AT1G59870	PEN3	plasma membrane ABC transporter, contributes to nonhost resistance to inappropriate pathogens that enter by direct penetration in a salicylic acid–dependent manner. Required for MLO resistance.	[35]
AT1G01720	ATAF1	putative transcriptional activator with NAC domain. Transcript level increases in response to wounding and abscisic acid.	[36]
AT1G61560	MILDEW RESISTANCE LOCUS O 6 (MLO6)	homolog of the barley mildew resistance locus o (MLO) protein, induced in response to a broad range of pathogens, confirmed co-expression with disease resistant protein encoding genes	[37] [38]
AT2G39200	MLO12	homolog of the barley mildew resistance locus o (MLO) protein, defense response to fungus, incompatible interaction	[39]
AT1G11310	MLO2	homolog of the barley mildew resistance locus o (MLO) protein, defense response to fungus, incompatible interaction	[39]
AT3G54920	POWDERY MILDEW RESISTANT 6 (PMR6)	Powdery mildew resistant mutant encodes a pectate lyase-like protein, defense response, incompatible interaction	[40]
AT5G58600	PMR5	Involved in resistance to the powdery mildew species Erysiphe cichoracearum and Erysiphe orontii, but not to the unrelated pathogens Pseudomonas syringae or Peronospora parasitica.	[41]
AT5G24530	DOWNY MILDEW	putative 2OG-Fe(II) oxygenase that is defense-associated but	[42]

	RESISTANT 6 (DMR6)	required for susceptibility to downy mildew,response to bacterium	
AT1G04750	VESICLE-ASSOCIATED MEMBRANE PROTEIN 721 (VAMP721)	forms part of plasma membrane SNARE PEN1-SNAP33-VAMP721/722 secretory complex that functions in plant defence	[43] [44] [45]
AT5G61210	SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33 (SNAP33)	Forms part of plasma membrane SNARE PEN1-SNAP33-VAMP721/722 secretory complex that functions in plant defence	[43] [46]
AT5G07880	SYNAPTOSOMAL-ASSOCIATED PROTEIN SNAP25-LIKE 29 (SNAP29)	SNAP receptor activity	[30]
AT1G13890	SNAP30	SNAP receptor activity	[30]
AT4G03550	GLUCAN SYNTHASE-LIKE 5 (ATGSL05), POWDERY MILDEW RESISTANT 4 (PMR4)	Encodes a callose synthase that is required for wound and papillary callose formation in response to fungal pathogens.. Contributes to PAMP-induced basal defense, callose deposition in cell wall during defense response	[17]
AT1G33960	AVRRPT2-INDUCED GENE 1 (AIG1)	induced by avirulence gene avrRpt2 and RPS2 after infection with Pseudomonas syringae carrying avrRpt2	[47]
AT3G28930	AVRRPT2-INDUCED GENE 2 (AIG2)	AVRRPT2-INDUCED GENE 2 (AIG2)	[47]
AT4G26090	RESISTANT TO P. SYRINGAE 2 (RPS2)	disease resistance protein (CC-NBS-LRR class). Encodes a plasma membrane protein that confers resistance to P syringae infection by interacting with the avirulence gene avrRpt2. RPS2 protein interacts directly with plasma membrane associated protein RIN4 and this interaction is disrupted by avrRpt2.	[48]
AT3G07040	RESISTANCE TO P. SYRINGAE PV MACULICOLA 1 (RPM1)	disease resistance protein(CC-NBS-LRR class), Confers resistance to P syringae strains that carry the avirulence genes avrB and avrRpm1.	[49]
AT3G25070	RPM1 INTERACTING PROTEIN 4 (RIN4)	Encodes a member of the R protein complex and may represent a virulence target of type III pili effector proteins (virulence factors) from bacterial pathogens, which is 'guarded' by R protein complex (RPM1 and RPS2 proteins).	[50]
AT5G45250	RESISTANT TO P. SYRINGAE 4 (RPS4)	Toll/interleukin-1 receptor (TIR)-nucleotide binding site (NBS)-LRR class of disease resistance (R) genes. Confers specific resistance to Pseudomonas syringae pv. tomato carrying the avirulence gene AvrRPS4.	[51]
AT1G12220	RESISTANT TO P. SYRINGAE 5 (RPS5)	Resistance gene, Confers resistance to Pseudomonas syringae strains that express avrPphB.	[52]
AT5G13160	avrPphB susceptible 1 (PBS1)	Mutant is defective in perception of Pseudomonas syringae avirulence gene avrPphB. Encodes a putative serine-threonine kinase.	[52]

AT5G14930	SENESCENCE-ASSOCIATED GENE 101 (SAG101),	EDS1-interacting acyl-hydrolase	[53 54]
AT1G33560	ACTIVATED DISEASE RESISTANCE 1 (ADR1)	Encodes a NBS-LRR disease resistance protein that possesses N-terminal kinase subdomains. Activation tagged mutant of ADR1 showed elevated levels of SA and reactive oxygen species in addition to number of defense gene transcripts. Exhibits resistance to number of microbial pathogens.	[55]
AT4G33300	ADR1-like 1 (ADR1-L1), putative disease resistance protein	disease resistance protein (CC-NBS-LRR class)	[56]
AT3G50480	HOMOLOG OF RPW8 4 (HR4)	RPW8 (RESISTANCE TO POWDERY MILDEW 8) is a disease resistance (R) gene involved in the recognition of a broad range of powdery mildew pathogens and induces localized SA-dependent defenses.	[57 58]
AT2G26560	PHOSPHOLIPASE A 2A (PLA2A)	Encodes a lipid acyl hydrolase with wide substrate specificity that accumulates upon infection by fungal and bacterial pathogens.	[59]
AT3G04720	PATHOGENESIS-RELATED 4 (PR4)	Encodes a protein similar to the antifungal chitin-binding protein hevein from rubber tree latex. mRNA levels increase in response to ETH and turnip crinkle virus infection.	[60]
AT3G12500	BASIC CHITINASE (CHIB)	encodes a basic chitinase involved in ETH/JAmediated signalling pathway during systemic acquired resistance defense response to fungus	[61]
AT4G11650	osmotin 34 (ATOSM34)	defense response to bacterium and fungas, incompatible interaction	[62]
AT1G73680	ALPHA DIOXYGENASE (ALPHA DOX2)	initiate the synthesis of oxylipin, pathogen-responsive alpha-dioxygenase, putative, response to other organism	[63]
AT1G21250	WAK1	may function as a signaling receptor of extracellular matrix component such as oligogalacturonides. expression induced by pathogens, or SA in an NPR1 dependent manner, required for resistance to lethal SA levels.	[64]
AT1G79680	WAKL10	Induced in response to a broad range of pathogens, confirmed co-expression with disease resistant protein encoding genes	[38]
AT1G79670	RESISTANCE TO FUSARIUM OXYSPORUM 1 (RFO1), WAKL22	A novel type of dominant disease-resistance protein that confers resistance to a broad spectrum of Fusarium races	[65]
AT5G47910	RESPIRATORY BURST OXIDASE HOMOLOGUE D (RBOHD)	Interacts with AtrbohF gene to fine tune the spatial control of ROI production and hypersensitive response to cell in and around infection site	[66]
AT1G64060	RESPIRATORY BURST OXIDASE PROTEIN F	Interacts with AtrbohD gene to fine tune the spatial control of ROI production and hypersensitive response to cell in and	[67]

	(ATRBOH F)	around infection site	
AT2G39940	CORONATINE INSENSITIVE 1 (COI1)	Required for wound- and jasmonates-induced transcriptional regulation, defense response to fungus	[68]
AT2G44050	COI1 SUPPRESSOR1 (COS1)	JA mediated signaling pathway	[69]
AT5G11270	OVEREXPRESSOR OF CATIONIC PEROXIDASE 3 (OCP3)	mediates resistance to infection by necrotrophic pathogens, JA mediated signaling pathway	[70]
AT2G46370	JASMONATE RESISTANT 1 (JAR1)	jasmonate-amino synthetase activity, catalyzes the formation of a biologically active jasmonyl-isoleucine (JA-Ile) conjugate, response to JA stimulus	[71]
AT5G42650	ALLENE OXIDE SYNTHASE (AOS)	JA biosynthetic pathway, defense response	[72 73]
AT2G06050	OPDA-REDUCTASE 3 (OPR3)	JA biosynthetic process	[74]
AT4G16760	ACYL-COA OXIDASE 1 (ACX1)	JA biosynthetic process	75
AT1G19640	JA CARBOXYL METHYLTRANSFERASE (JMT)	JA biosynthetic process	76
AT1G19670	CORONATINE-INDUCED PROTEIN 1 (ATCLH1),	Chlorophyllase 1, chlorophyll catabolic process, response to stress and JA stimulus	77
AT4G23600	CORONATINE INDUCED 1 (CORI3)	generation of precursors of ETH biosynthesis, response to JA stimulus	[78 79]
AT1G75830	PLANT DEFENSIN 1.2 (PDF1.1) / LOW-MOLECULAR-WEIGHT CYSTEINE-RICH 67 (LCR67)	Predicted to encode a PR (pathogenesis-related) protein, belongs to the plant defensin (PDF) family protein, defense response	[80]
AT2G26020	PDF1.2b	As above	[80]
AT1G19610	PDF1.4 / LCR78	As above	[80]
AT2G02120	PDF2.1 / LCR70	As above	[80]
AT2G02100	PDF2.2 / LCR69	As above	[80]
AT2G02130	PDF2.3 / LCR68	As above	[80]
AT1G61070	PDF2.4 / LCR66	As above	[80]
AT5G63660	PDF2.5 / LCR74	As above	[80]
AT2G02140	PDF2.6 / LCR72	As above	[80]
AT5G38330	LCR80	As above	[80]

AT5G44420	PDF1.2 / LCR77	Encodes an ETH- and jasmonate-responsive plant defensin. mRNA levels are not responsive to SA treatment; although jasmonate and SAcan act synergistically to enhance the expression of this gene. Belongs to the plant defensin (PDF) family.	[81 82]
AT1G72260	THIONIN 2.1 (THI2.1)	Encodes a thionin which is a cysteine rich protein having antimicrobial properties. Thi2.1 is expressed in response to a variety of pathogens and induced by ETH and JA Belongs to the plant thionin (PR-13) family	[83]
AT5G36910	THIONIN 2.2 (THI2.2)	Predicted to encode a PR, belongs to the plant defensin (PDF) family protein, defense response defense response	[80]
AT2G33150	PEROXISOMAL 3-KETOACYL-COA THIOLASE 3 (PKT3), KAT 2	JA biosynthetic process	[84 85]
AT1G04710	PKT4	acetyl-CoA C-acyltransferase	[84 85]
AT4G23570	SGT1A,	Closely related to SGT1B, may function in SCF(TIR1) mediated protein degradation. AtSGT1a and AtSGT1b are functionally redundant in the resistance to pathogens.	[86]
AT4G11260	SGT1B	as above, required for defense signaling conferred by several downy mildew resistance genes, JA mediated signaling pathway	[87]
AT5G48485	DEFECTIVE IN INDUCED RESISTANCE 1 (DIR1)	encodes a putative apoplastic lipid transfer protein that is involved in SAR	[88]
AT3G45640	MITOGEN-ACTIVATED PROTEIN KINASE 3 (MPK3)	Functions in MAP kinase cascade involving MEKK1, MKK4/MKK5 and MPK3/MPK6 that functions downstream of the FLS2 fagellin receptor, activation of this MAPK cascade confers resistance to both bacterial and fungal pathogens	[89 90]
AT4G01370	MPK4	nuclear and cytoplasmically localized MAP kinase, regulates SA and jasmonic acid/ETH-dependent responses via EDS1 and PAD4	[91]
AT2G43790	MPK6	as MPK3	[89 92]
AT4G26070	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MKK1) / MEK1 (MAP KINASE/ ERK KINASE 1)	Shares functional redundancy with MKK1/2, involved in jasmonate- and salicylate-dependent defense responses	[93]
AT4G29810	MKK2	Shares functional redundancy with MKK1/2, involved in jasmonate- and salicylate-dependent defense responses	[93]
AT1G51660	MKK4	as MPK3	[89]
AT3G21220	MKK5	as MPK3	[89]
AT1G08720	ENHANCED DISEASE RESISTANCE 1 (EDR1); MAP kinase kinase kinase/ kinase/ protein serine/threonine/tyrosine	confers resistance to powdery mildew disease caused by the fungus Erysiphe cichoracearum, response to bacterium and fungus	[23 24]

	kinase		
AT1G73500	MAP KINASE KINASE 9 (MKK9)	Autophosphorylates and also phosphorylates MPK3 and MPK6. Independently involved in ETH and calmalexin biosynthesis. Induces transcription of ACS2, ACS6, ERF1, ERF2, ERF5, ERF6, CYP79B2, CYP79B3, CYP71A13 and PAD3.	[94]
AT3G06110	MAPK PHOSPHATASE 2 (MKP2)	nuclear-localized MAPK phosphatase. Plants with reduced levels of MKP2 transcripts are hypersensitive to ozone and ozone-mediated activation of MPK3 and MPK6 is prolonged in these plants.	[95]
AT5G53210	SPEECHLESS (SPCH)	SPCH is a substrate of a kinase MPK3 and MPK6	[96]
AT1G10210	MITOGEN-ACTIVATED PROTEIN KINASE 1 (ATMPK1)	Activated by wounding JA	[97]
AT1G18350	MAP KINASE KINASE7 (ATMKK7)	defense response to bacterium, positively regulates plant basal and systemic acquired resistance (SAR)	[98]
AT4G08500	MAP KINASE KINASE KINASE 1 (MEKK1)	as MPK3	[89 99]
AT1G19180	JASMONATE-ZIM-DOMAIN PROTEIN 1 (JAZ1); (TIFY10A)	nuclear-localized protein involved in jasmonate signaling, induced by jasmonate	[100 101 102]
AT1G74950	JAZ2/TIFY10B	response to JA stimulus and wounding	[102 103]
AT3G17860	JAZ3	negatively regulates the key transcriptional activator of JA responses, AtMYC2, induced by jasmonate	[100 102]
AT5G13220	JAZ10	induced by jasmonate, regulation of systemic acquired resistance	[104 105]
AT1G32640	MYC2	MYC-related transcriptional activator, regulates diverse JA-dependent functions.	[81]
AT4G17500	ETH RESPONSIVE ELEMENT BINDING FACTOR 1 (ATERF-1)	member of the ERF (ETH response factor) subfamily B-3 of ERF/AP2 transcription factor family, response to chitin	[26]
AT3G23240	ETH RESPONSE FACTOR 1 (ERF1)	member of the ERF subfamily B-3 of ERF/AP2 transcription factor Involved in ETH signaling cascade,downstream of EIN2 and EIN3.	[106]
AT3G16770	ETH-RESPONSIVE ELEMENT BINDING PROTEIN (ATEBP)	member of the ERF subfamily B-3, part of the ETH signaling pathway and is predicted to act downstream of EIN2 and CTR1, but not under EIN3. response to other organism, ETH mediated signaling pathway	[107]
AT3G15210	ETH RESPONSIVE ELEMENT BINDING FACTOR 4 (ERF4)	member of the ERF subfamily of transcription factors, negative regulator of JA-responsive defense gene expression and resistance to the necrotrophic fungal pathogen Fusarium oxysporum and antagonizes JA inhibition of root elongation	[108]

AT5G03280	ETH INSENSITIVE 2 (EIN2)	Involved in ETH signal transduction. Acts downstream of CTR1, defense response to fungus	[109]
AT1G66340	ETH RESPONSE 1 (ETR1)	ETH receptor, defense response to bacterium	[110]
AT2G19560	ENHANCED ETH RESPONSE 5 (EER5)	encodes a protein with a PAM domain involved in ETH signaling.	[111]
AT2G26070	REVERSION-TO-ETH SENSITIVITY1 (RTE1)	appears to be involved in the negative regulation of the response to ETH, is localized to the Golgi and is a positive regulator of ETR1.	[112]
AT4G31550	WRKY11	negative regulator of basal resistance	[113]
AT2G23320	WRKY15	response to chitin	[26]
AT4G31800	WRKY18	Pathogen-induced transcription factor, forms protein complexes with itself and with WRKY40 and WRKY60. WRKY18, -40, and -60 have partially redundant roles in response to the hemibiotrophic bacterial pathogen P. syringae and the necrotrophic fungal pathogen B cinerea, with WRKY18 playing a more important role than the other two.	[114 115] [116]
AT4G01250	WRKY22	Functions redundantly with WRKY29 in activating early-defence genes, involved in bacterial and fungal defence responses	[87]
AT4G18170	WRKY28	Induced in response to a broad range of pathogens, confirmed co-expression with disease resistant protein encoding genes	[38]
AT2G38470	WRKY33	Regulates the antagonistic relationship between defense pathways mediating responses to P. syringae and necrotrophic fungal pathogens	[117]
AT1G80840	WRKY40	As WRKY18	[114]
AT2G25000	WRKY60	As WRKY18	[114 115]
AT3G56400	WRKY70	Function as activator of SA-dependent defense genes and a repressor of JA-regulated genes. WRKY70-controlled suppression of JA-signaling is partly executed by NPR1	[118]

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